

SEQ ID NO:4 Sequence Comparison A

AAR55367
 ID AAR55367 standard; Protein; 509 AA.
 XX
 AC AAR55367;
 XX
 DT 20-JAN-1995 (first entry)
 XX
 DE Human Activin receptor-like kinase 2 (hALK-2).
 XX
 KW serine threonine kinases; activin receptors; Act-R; superfamily;
 KW transforming growth factor; TGF; diagnostics; detection; therapy;
 KW rheumatoid arthritis; glomerular nephritis; fibrosis.
 XX
 OS Homo sapiens.
 XX
 PN WO9411502-A.
 PS Claim 3; Page 40-43; 97pp; English.
 SQ Sequence 509 AA;

Query Match 100.0%; Score 621; DB 15; Length 509;
 Best Local Similarity 100.0%; Pred. No. 2.4e-54;
 Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPSPSMEDEKPKVNPPLYMCVCEGLSCGNEDHCEGQQCFSSLSINDGFHVYQKGCQVVE 60
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 Db 16 LPSPSMEDEKPKVNPPLYMCVCEGLSCGNEDHCEGQQCFSSLSINDGFHVYQKGCQVVE 75
 QY 61 QGKMTCKTPPSPGQAVECCQGDWCNRNITAQLPTKGKSFPGTQNFHLE 108
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 Db 76 QGKMTCKTPPSPGQAVECCQGDWCNRNITAQLPTKGKSFPGTQNFHLE 123

Sequence Comparison B

A45992
 activin A receptor type I - human
 N;Alternate names: activin A receptor type II-like kinase 2; ALK-2;
 serine/threonine kinase-type receptor SKR1
 C;Species: Homo sapiens (man)
 C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 24-Sep-1999
 C;Accession: A45992; I37162; S37182
 R;Matsuzaki, K.; Xu, J.; Wang, F.; McKeehan, W.L.; Krummen, L.; Kan, M.
 J. Biol. Chem. 268, 12719-12723, 1993
 A;Title: A widely expressed transmembrane serine/threonine kinase that does
 not bind activin, inhibin, transforming growth factor beta, or bone
 morphogenic factor.
 A;Reference number: A45992; MUID:93286114; PMID:8389764
 A;Accession: A45992
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-509 <MAT>
 A;Cross-references: GB:L02911; NID:g338218; PIDN:AAA36614.1; PID:g338219
 R;ten Dijke, P.; Ichijo, H.; Franzen, P.; Schulz, P.; Saras, J.; Toyoshima,
 H.; Heldin, C.H.; Miyazono, K.

0;

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Qy      1 QNLD SMLHGTGMKSDSDQKKSENGVTLAPEDTL PFLKCYCSGHC PDDAINNTCITNGHCF 60
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Qy      61 AII EEDDQGETTLASGCMKYEGSDFQCKDSPKAQLRRTIECCRTNLCNQYLQPTLPPVVI 120
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Db      84 AII EEDDQGETTLASGCMKYEGSDFQCKDSPKAQLRRTIECCRTNLCNQYLQPTLPPVVI 143

Qy      121 GPFFDGSIR 129
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Db      144 GPFFDGSIR 152

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Sequence Comparison D

I37163
 ALK-3 - human
 C;Species: Homo sapiens (man)
 C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 24-Sep-1999
 C;Accession: I37163; S37183
 R;ten Dijke, P.; Ichijo, H.; Franzen, P.; Schulz, P.; Saras, J.; Toyoshima, H.; Heldin, C.H.; Miyazono, K.
Oncogene 8, 2879-2887, 1993
 A;Title: Activin receptor-like kinases: a novel subclass of cell-surface receptors with predicted serine/threonine kinase activity.
 A;Reference number: I37161; MUID:93390967; PMID:8397373
 A;Accession: I37163
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: mRNA
 A;Residues: 1-532 <RES>
 A;Cross-references: EMBL:Z22535; NID:g402186; PIDN:CAA80257.1; PID:g402187
 C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homology
 C;Keywords: ATP
 F;232-528/Domain: protein kinase homology <KIN>
 F;240-248/Region: protein kinase ATP-binding motif

Query Match 100.0%; Score 715; DB 2; Length 532;
 Best Local Similarity 100.0%; Pred. No. 8.7e-58;
 Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 QNLD SMLHGTGMKSDSDQKKSENGVTLAPEDTL PFLKCYCSGHC PDDAINNTCITNGHCF 60
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Qy      61 AII EEDDQGETTLASGCMKYEGSDFQCKDSPKAQLRRTIECCRTNLCNQYLQPTLPPVVI 120
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Qy      121 GPFFDGSIR 129
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Db      144 GPFFDGSIR 152

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SEQ ID NO:8

Sequence Comparison E

ID AAR55374 standard; Protein; 502 AA.
 XX
 AC AAR55374;
 XX
 DT 20-JAN-1995 (first entry)
 XX
 DE Mouse Activin receptor-like kinase 6 (mALK-6).
 XX
 KW serine threonine kinases; activin receptors; Act-R; superfamily;
 KW transforming growth factor; TGF; diagnostics; detection; therapy;
 KW rheumatoid arthritis; glomerular nephritis; fibrosis.
 XX
 OS Mus musculus.
 XX
 PN WO9411502-A.
 XX
 PD 26-MAY-1994.
 XX
 PF 17-NOV-1993; 93WO-GB02367.
 XX
 PR 17-NOV-1992; 92GB-0024057.
 PR 08-MAR-1993; 93GB-0004677.
 PR 08-MAR-1993; 93GB-0004680.
 PR 28-MAY-1993; 93GB-0011047.
 PR 02-JUL-1993; 93GB-0013763.
 PR 03-AUG-1993; 93GB-0016099.
 PR 15-OCT-1993; 93GB-0021344.
 XX
 PA (LUDW-) LUDWIG INST CANCER RES.
 XX
 PI Dijke P, Franzen P, Heldin C, Miyazono K, Yamashita H;
 XX
 DR WPI; 1994-183503/22.
 DR N-PSDB; AAQ66642.
 XX
 PS Claim 3; Page 75-77; 97pp; English.
 XX
 SQ Sequence 502 AA;

Query Match 100.0%; Score 581; DB 15; Length 502;
 Best Local Similarity 100.0%; Pred. No. 1.1e-50;
 Matches 100; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PTPRPKILRCKCHHHCPEDSVNNICSTDGYCFTMIEEDDSGMPVVTSGCLGLEGSDFQCR 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 23 PTPRPKILRCKCHHHCPEDSVNNICSTDGYCFTMIEEDDSGMPVVTSGCLGLEGSDFQCR 82
 Qy 61 DTPIPHQRRSIECCTERNECNKDLHPTLPPLKDRDFVDGP 100
 ||||||||||||||||||||||||||||||||||||||||||||
 Db 83 DTPIPHQRRSIECCTERNECNKDLHPTLPPLKDRDFVDGP 122

A53444

C;Species: Mus musculus (house mouse)

C;Accession: A53444; S40159

Science 264, 101-104, 1994

A;Reference number: A53444; MUID:94188705; PMID:8140412

A;Status: preliminary

A;Residues: 1-502 <TEN>

R;Miyazono, K.; Moren, A.; Grimsby, S.; Ichijo, H.; Heldin, C.; ten Dijke, P.
submitted to the EMBL Data Library, June 1993

A;Reference number: S40158

A;Status: preliminary

A;Residues: 1-502 <MIY>

C; Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homology

F;202-498/Domain: protein kinase homology <KIN>

F;210-218/Region: protein kinase ATP-binding motif

Best Local Similarity 100.0%; Pred. No. 1.8e-46;

Matches 100; Conservative 0; Mismatches 0; Indels 0; Gaps

0;

Db 23 PTPRPKILRCKCHHHCPEDSVNNICSTDGYCFTMIEEDDSGMPVVTSGCLGLEGSDFQCR 82

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Db 83 DTPIPHQRRSIECCTERNECNKDLHPTLPPLKDRDFVDGP 122

SEQ ID NO:12

Sequence Comparison G

ID AAQ66643 standard; cDNA; 28 BP.
XX
AC AAQ66643;
XX
DT 20-JAN-1995 (first entry)
XX
DE Primer B1-S to generate a probe for Activin receptor-like kinase
cDNA.
XX
OS Synthetic.
XX
PN WO9411502-A.
XX
PD 26-MAY-1994.
XX
PS Disclosure; Page 79; 97pp; English.
XX
SQ Sequence 28 BP; 6 A; 4 C; 10 G; 8 T; 0 other;

Query Match 96.4%; Score 27; DB 15; Length 28;
Best Local Similarity 96.4%; Pred. No. 0.0058;
Matches 27; Conservative 0; Mismatches 1; Indels 0;
Gaps 0;

Qy 1 GCGGATCCTGTTGTGAAGGNAATATGTG 28
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Db 1 GCGGATCCTGTTGTGAAGGCAATATGTG 28

SEQ ID NO:13

Sequence Comparison H

ID AAQ66644 standard; cDNA; 24 BP.
XX
AC AAQ66644;
XX
DT 20-JAN-1995 (first entry)
XX
DE Primer B3-S to generate a probe for Activin receptor-like kinase
cDNA.
XX
OS Synthetic.
XX
PN WO9411502-A.
XX
PD 26-MAY-1994.
XX
PI Dijke P, Franzen P, Heldin C, Miyazono K, Yamashita H;
XX
DR WPI; 1994-183503/22.
XX
XX
PS Disclosure; Page 80; 97pp; English.
XX

SQ Sequence 24 BP; 6 A; 6 C; 5 G; 7 T; 0 other;

Query Match 100.0%; Score 24; DB 15; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.0094;
Matches 24; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;

QY 1 GCGATCCGTCGCAGTCAAAATTTT 24
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Db 1 GCGATCCGTCGCAGTCAAAATTTT 24

Sequence Comparison I

SEQ ID NO:14

ID AAQ66645 standard; cDNA; 26 BP.
XX
AC AAQ66645;
XX
DT 20-JAN-1995 (first entry)
XX
DE Primer B7-S to generate a probe for Activin receptor-like kinase
cDNA.
OS Synthetic.
XX
PN WO9411502-A.
XX
PD 26-MAY-1994.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Dijke P, Franzen P, Heldin C, Miyazono K, Yamashita H;
XX
DR WPI; 1994-183503/22.
XX
PS Disclosure; Page 80; 97pp; English.
XX
SQ Sequence 26 BP; 10 A; 5 C; 6 G; 5 T; 0 other;

Query Match 100.0%; Score 26; DB 15; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.005;
Matches 26; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;

QY 1 GCGGATCCGCGATATATTTAAAGCAA 26
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Db 1 GCGGATCCGCGATATATTTAAAGCAA 26

SEQ ID NO:15

ID AAQ66646 standard; cDNA; 20 BP.
XX
AC AAQ66646;
XX
DT 20-JAN-1995 (first entry)
XX
DE Primer E8-AS to generate a probe for Activin receptor-like kinase
cDNA.
XX
OS Synthetic.
XX
PN WO9411502-A.
XX
PD 26-MAY-1994.
XX
PF 17-NOV-1993; 93WO-GB02367.
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Dijke P, Franzen P, Heldin C, Miyazono K, Yamashita H;
XX
DR WPI; 1994-183503/22.
XX
PS Disclosure; Page 80; 97pp; English.
SQ Sequence 20 BP; 5 A; 4 C; 5 G; 6 T; 0 other;

Query Match 100.0%; Score 20; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.93;
Matches 20; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;

Qy 1 CGGAATTCTGGTGCCATATA 20
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Db 1 CGGAATTCTGGTGCCATATA 20

SEQ ID NO:7

Sequence Comparison K

LOCUS MMALK6A 1944 bp mRNA linear ROD 13-MAY-1994
 DEFINITION M.musculus ALK-6 mRNA, complete CDS.
 ACCESSION Z23143
 VERSION Z23143.1 GI:437870
 KEYWORDS ALK-6 gene; serine/threonine kinase receptor.
 SOURCE Mus musculus.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 1944)
 AUTHORS ten Dijke, P., Yamashita, H., Ichijo, H., Franzen, P., Laiho, M.,
 Miyazono, K. and Heldin, C.H.
 TITLE Characterization of type I receptors for transforming growth
 factor-beta and activin
 JOURNAL Science 264 (5155), 101-104 (1994)
 MEDLINE 94188705
 PUBMED 8140412
 REFERENCE 2 (bases 1 to 1944)
 AUTHORS Miyazono, K.
 TITLE Direct Submission
 JOURNAL Submitted (25-JUN-1993) Kohei Miyazono, Ludwig Institute for
 Cancer
 Research, Biomedical, Center, Uppsala, S-751 24, Sweden
 FEATURES Location/Qualifiers
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 /strain="NIH Swiss"
 /db_xref="taxon:10090"
 /clone="ME-6"
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 /dev_stage="12 day embryo"
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 /codon_start=1
 /product="ALK-6"
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 PSFPNRWSSDECLRQMGKLMTECWAQNPASRLTALRVKKT LAKMSESQDIKL"
 sig_peptide 187. .225
 mat_peptide 226. .1692
 /product="ALK-6"
 BASE COUNT 546 a 446 c 503 g 449 t
 ORIGIN
 Query Match 100.0%; Score 297; DB 10; Length 1944;
 Best Local Similarity 100.0%; Pred. No. 4.2e-85;
 Matches 297; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACCCCTCGGCCCAAGATCCTACGTTGTAAATGCCACCACCCTGTCCGGAAGACTCAGTC 60
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 Db 256 ACCCCTCGGCCCAAGATCCTACGTTGTAAATGCCACCACCCTGTCCGGAAGACTCAGTC 315
 Qy 61 AACAAATATCTGCAGCACAGATGGGTACTGCTTCACGATGATAGAAGAAGATGACTCTGGA 120
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 Db 316 AACAAATATCTGCAGCACAGATGGGTACTGCTTCACGATGATAGAAGAAGATGACTCTGGA 375
 Qy 121 ATGCCTGTTGTCACCTCTGGATGTCTAGGACTAGAAGGGTCAGATTTTCAATGTCGTGAC 180
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 Db 376 ATGCCTGTTGTCACCTCTGGATGTCTAGGACTAGAAGGGTCAGATTTTCAATGTCGTGAC 435
 Qy 181 ACTCCCATTCCTCATCAAAGAAGATCAATTGAATGCTGCACAGAAAGGAATGAGTGTAAT 240
 |||
 Db 436 ACTCCCATTCCTCATCAAAGAAGATCAATTGAATGCTGCACAGAAAGGAATGAGTGTAAT 495
 Qy 241 AAAGACCTCCACCCCACTCTGCCTCCTCTCAAGGACAGAGATTTTGTGTGATGGGCCC 297
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 Db 496 AAAGACCTCCACCCCACTCTGCCTCCTCTCAAGGACAGAGATTTTGTGTGATGGGCCC 552

ID AAQ66642 standard; cDNA; 1952 BP. *Sequence Comparison L*
 XX
 AC AAQ66642;
 XX
 DT 20-JAN-1995 (first entry)
 OS Mus musculus.
 XX
 FH Key Location/Qualifiers
 FT 5'UTR 1..186
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 FT /note= "contains an in-frame stop codon at
 FT nucleotides 163-165"
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 FT /*tag= b
 FT /product= activin receptor-like kinase 6
 FT 3'UTR 1696..1952
 FT /*tag= c
 FT /note= "there is no polyA signal indicating that
 FT the cDNA was internally primed"
 XX
 PN WO9411502-A.
 XX
 PD 26-MAY-1994.
 XX
 PA (LUDW-) LUDWIG INST CANCER RES.
 XX
 PI Dijke P, Franzen P, Heldin C, Miyazono K, Yamashita H;
 XX
 PS Claim 21; Page 75-77; 97pp; English.
 XX
 SQ Sequence 1952 BP; 554 A; 448 C; 501 G; 449 T; 0 other;
 Query Match 100.0%; Score 297; DB 15; Length 1952;
 Best Local Similarity 100.0%; Pred. No. 2.7e-88;

Matches 297; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 ACCCCTCGGCCCAAGATCCTACGTTGTAAATGCCACCACCACCTGTCCGGAAGACTCAGTC 60
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Db    256 ACCCCTCGGCCCAAGATCCTACGTTGTAAATGCCACCACCACCTGTCCGGAAGACTCAGTC 315

Qy     61 AACAAATATCTGCAGCACAGATGGGTACTGCTTCACGATGATAGAAGAAGATGACTCTGGA 120
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    316 AACAAATATCTGCAGCACAGATGGGTACTGCTTCACGATGATAGAAGAAGATGACTCTGGA 375

Qy    121 ATGCCTGTTGTCACCTCTGGATGTCTAGGACTAGAAGGGTCAGATTTTCAATGTCGTGAC 180
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    376 ATGCCTGTTGTCACCTCTGGATGTCTAGGACTAGAAGGGTCAGATTTTCAATGTCGTGAC 435

Qy    181 ACTCCCATTCCCTCATCAAAGAAGATCAATTGAATGCTGCACAGAAAGGAATGAGTGTAAT 240
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    436 ACTCCCATTCCCTCATCAAAGAAGATCAATTGAATGCTGCACAGAAAGGAATGAGTGTAAT 495

Qy    241 AAAGACCTCCACCCCACTCTGCCTCCTCTCAAGGACAGAGATTTTGTGTTGATGGGCCC 297
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    496 AAAGACCTCCACCCCACTCTGCCTCCTCTCAAGGACAGAGATTTTGTGTTGATGGGCCC 552
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